secreted with a second copy of C_H3 expressed from the natural gene (Ellison et al. Nucleic Acids Res. 10:4071-4079 (1982)) as a fusion protein with M13 gene III protein. The synthetic C_H3 gene is preceded by a sequence encoding a peptide derived from herpes simplex virus glycoprotein D (gD flag, Lasky, L. A. and Dowbenko, D. J. (1984) DNA 3:23-29; Berman, P. W. *et al.*, (1985) Science 227:1490-1492 and a cleavage (G) site for the site-specific protease, Genenase I (Carter, P. *et al.* (1989) Proteins: Structure, Function and Genetics 6:240-248). Fig. 2C is the nucleic acid sequence of the dicistronic operon (SEQ ID NO:13) of Fig. 2B in which the residues in the translated C_H3 genes are numbered according to the Eu system of Kabat et al. In Sequences of Proteins of Immunological Interest, 5th ed. vol. 1, pp. 688-696, NIH, Bethesda, MD (1991). Protuberance mutation T366W is shown, as are the residues targeted for randomization in the natural C_H3 gene (366, 368, and 407).--

Please replace the paragraph beginning at page 95, line 29, with the following rewritten paragraph:

--A large human single chain Fv (scFv) antibody library (Vaughan *et al.* (1996), *supra*) was panned for antibodies specific for eleven antigens including Axl(human receptor tyrosine kinase ECD), GCSF-R (human granulocyte colony stimulating factor receptor ECD), IgE (murine IgE), IgE-R (human IgE receptor α-chain), MPL (human thrombopoietin receptor tyrosine kinase ECD), MusK (human muscle specific receptor tyrosine kinase ECD), NpoR (human orphan receptor NpoR ECD), Rse (human receptor tyrosine kinase, Rse, ECD), HER3 (human receptor tyrosine kinase HER3/c-erbB3 ECD), Ob-R (human leptin receptor ECD), and VEGF (human vascular endothelial growth factor) where ECD refers to the extracellular domain. The nucleotide sequence data for scFv fragments from populations of antibodies raised to each antigen was translated to derive corresponding protein sequences. The V_L sequences were then compared using the program "align" with the algorithm of Feng and Doolittle (1985, 1987, 1990) to calculate the percentage identity between all pairwise combinations of chains (Feng, D.F. and Doolittle, R.F. (1985) J. Mol. Evol. 21:112-123; Feng, D.F. and Doolittle, R.F. (1987) J. Mol. Evol. 25:351-360; and Feng, D.F. and Doolittle, R.F. (1990) Methods Enzymol. 183:375-387). The percent sequence identity results of each pairwise light chain amino acid sequence comparison were arranged in matrix format (see Table 6.1-6.15).--

Please amend the specification by renumbering pages 104-111 to be pages 116-123. Please further amend the specification by inserting after page 103 the attached Sequence Listing as pages 104-115.